

MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPCPGTFVQR
PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF
AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPGTFSASSSSSEQCQPHRNCTALGLA
LNVPGSSSHDTLCTSGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE
GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLQLRVARMPGLERSVRERFLPVH

Fig. 1

09896096-062804

TCCGCGCTGAGCCGCGCTCTCCCTGCTCCAGCAAGGACC

TCCGCGAGGCGGACCGGGGGCAAAGGAGGTGGCATGTCCGGTCAGGCACAGCAGGGTCCTGT
GTCCGCGCTGAGCCGCGCTCTCCCTGCTCCAGCAAGGACC
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ATGAGGGCGCTGGAGGGGCCAGGCCTGTGCTGCTGTGCCTGGTGTGGCGCTGCCTGCC
CTGCTGCCGGTGCCGGCTGTACGCGGAGTGGCAGAAACACCCACCTACCCCTGGCGGGAC
GCAGAGACAGGGGAGCGGCTGGTGTGCGCCAGTGCCCCCAGGCACCTTTGTGCAGCGG
CCGTGCCGCGGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACGCAG
TTCTGGAACCTACCTGGAGCGCTGCCGCTACTGCAACGTCTCTGCGGGGAGCGTGAGGAG
GAGGCACGGGCTTGCCACGCCACCCACAACCGTGCTGCCGCTGCCGCACCGGCTTCTTC
GCGCACGCTGGTTTCTGCTTGAGACACGCATCGTGTCCACCTGGTGCCGGCGTGATTGCC
CCGGGCACCCCCAGCCAGAACACGCAGTGCCAGCCGTGCCCCCAAGGCACCTTCTCAGCC
AGCAGCTCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCTGGCC
CTCAATGTGCCAGGCTCTTCTCCCATGACACCCCTGTGCACCAGCTGCACTGGCTTCCCC
CTCAGCACCAGGGTACCAGGAGCTGAGGAGTGTGAGCGTGCCGTCATCGACTTTGTGGCT
TTCCAGGACATCTCCATCAAGAGGCTGCAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAG
GGCTGGGGTCCGACACCAAGGGCGGGCCGCGCGGCTTGCAGCTGAAGCTGCGTCGGCGG
CTCACGGAGCTCCTGGGGGCGCAGGACGGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTG
CGCGTGGCCAGGATGCCCGGGCTGGAGCGGAGCGTCCGTGAGCGCTTCTCCCTGTGCAC
TGATCCTGGCCCCCTCTTATTTATTCTACATCCTTGGCACCCCACTTGCACTGAAAGAGG
CTTTTTTTTTAAATAGAAGAAATGAGGTTTNTTAAAAAAAAAAAAAAAAAAAAA

Fig. 2

09896096-062801

GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACG
CAGTTCTGGAANTAACTGGAGCNCTGCCGCTACTGNAACGTCCTCTGNNG
GGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCACAACCGTGCCT
GCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC
GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCA
GAACACGCAGTGCCCTAGCCGTGCCCCCAGGCACCTTCTCAGCCAGCAGC
TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCT
GGCCCTCAATGTGCCAGGCTCTTCCTCCCATGACACCCTGTGCACCAGCT
GCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAGGAGTGTGAG
CGTGCCGTCATCGACTTTGTGGCTTTCAGGACATCTCCAT

Fig. 3

SEQ ID NO: 4 128 GCCGAGACAGCCCAACGACGTGTGGCCCGTGTCCACCGCGCCACTACACG
 SEQ ID NO: 5 1 GCCGAGACAGCCCAACGACGTGTGGCCCGTGTCCACCGCGCCACTACACG
 SEQ ID NO: 6 1
 SEQ ID NO: 3 1 GCCGAGACAGCCCAACGACGTGTGGCCCGTGTCCACCGCGCCACTACACG

SEQ ID NO: 4 178 CA-TTCTGGAACCTACCTGGAGCGC
 SEQ ID NO: 5 51 CAGTTCTGGAANTAACTGGAGCNCCTGCCGCTACTGNAACGTCCTCTGNGG
 SEQ ID NO: 6 2 CAGTTCTGGAACCTACCTGGAGCGCTGCCGCTACTGCAACGTCCTCTGCGG
 SEQ ID NO: 3 51 CAGTTCTGGAANTAACTGGAGCNCCTGCCGCTACTGNAACGTCCTCTGNGG

SEQ ID NO: 5 101 GGAGCNTGAGGAGGAGGCANGNGCTTGCCACGCCACCCACAACCGCGCCT
 SEQ ID NO: 6 52 GGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCACAACCGTGCCCT
 SEQ ID NO: 7 1 GAGGGGCCCCCAGGAGTGTTGCCACGCCACCCACAACCGTGCCCT
 SEQ ID NO: 3 101 GGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCACAACCGTGCCCT

SEQ ID NO: 5 151 GCNGCTGCAGACCGGNTTCTTCGCGCACGCTGNTTCTGCTTGGAGCAC
 SEQ ID NO: 6 102 GCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC
 SEQ ID NO: 7 32 TGGCAGGGGTACAGTTGCTGGTCCCAGCCTTGACCCCTGAGCTAGGACAC
 SEQ ID NO: 3 151 GCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC

SEQ ID NO: 5 201 GCATCGTGTCCACCTGGTGNCGGCGTGATTGCNCCGGGCACCCCCAGCCA
 SEQ ID NO: 6 152 GCATCGTGTCCACCTGGTGC CGCGGTGATTNCCCGGGCACCCCCAGCCA
 SEQ ID NO: 7 82 CAGTTCCCTGACCCCTGTTCTTCCCTCCTGGCTGCAGGCACCCCCAGCCA
 SEQ ID NO: 8 1 GCATCGTGTCCACCTGGTGC CGCGGTGATTGCCCCGGGCACCCCCAGCCA
 SEQ ID NO: 10 1 CTTGTCCACCTGGTGC CGCGGTGATTNCCC-GGGACCCCCAGCCA
 SEQ ID NO: 3 201 GCATCGTGTCCACCTGGTGC CGCGGTGATTGCCCCGGGCACCCCCAGCCA

Fig. 4

SEQ ID NO: 5 251 GAACACGCA - TGCAAAGCCGTG
 SEQ ID NO: 7 132 GAACACGAGN - CC - AGCCGTGCCCCCAGGCACCTTCTCAGCCAGCAGC
 SEQ ID NO: 8 51 GAACACGAG - GCCTAGCCGTGCCCCCAGGCACCTTCTCAGCCAGCAGC
 SEQ ID NO: 10 47 GAACACGAGTGC - AGCNT - CCCCCAGGCACCTTCTCAGCCAGCAGC
 SEQ ID NO: 9 1 AGCNGTGCCNCCNAGGCACCTTCTCAGCCAGCAGT
 SEQ ID NO: 3 251 GAACACGAGTGCCTAGCCGTGCCCCCAGGCACCTTCTCAGCCAGCAGC

 SEQ ID NO: 7 182 TCCAGCTCAGAGCAGTGCCAGCCCCACCGAACTGCACGGCCCTGGGCCT
 SEQ ID NO: 8 101 TCCAGCTCAGAGCAGTGCCAGCCCCACCGAACTGCACGGCCCTGGGCCT
 SEQ ID NO: 10 97 TCCAGCTCAGAGCAGTGCCAGCCCCACCGAACTGCACGGCCCTGGNC - T
 SEQ ID NO: 9 36 TCCAGCTCAGAGCAGTGCCAGCCCCACCGAACTGCACGGCCCTGGGCCT
 SEQ ID NO: 3 301 TCCAGCTCAGAGCAGTGCCAGCCCCACCGAACTGCACGGCCCTGGGCCT

 SEQ ID NO: 7 232 GGCCCTCAATGTGCCAGGCTCTTCTCCCATGACACCCCTGTGCACCCAG
 SEQ ID NO: 8 151 GGCCCTCAATGTGCCAGGCTCTTCTCCCATGACACCCCTGTGCACCCAGCT
 SEQ ID NO: 10 147 GGCCCTCAATGTGCCAGGCTCTTCTCCCATGACACCCCTGTGCACCCAGCT
 SEQ ID NO: 9 86 GGCCCTCAATGTGCCAGGCTCTTCTCCCATGACACCCCTGTGCACCCAGCT
 SEQ ID NO: 3 351 GGCCCTCAATGTGCCAGGCTCTTCTCCCATGACACCCCTGTGCACCCAGCT

 SEQ ID NO: 10 197 GCACTGGCTTCCCCCTCAGCACCCAGGTACCAGGAGCTGAGGAGTGTGAG
 SEQ ID NO: 9 136 GCACTGGCTTCCCCCTCAGCACCCAGGTACCAGGAGCTGAGGAGTGTGAG
 SEQ ID NO: 3 401 GCACTGGCTTCCCCCTCAGCACCCAGGTACCAGGAGCTGAGGAGTGTGAG

 SEQ ID NO: 10 247 CGTGCCGTCATCGACTTTGTGGCTTCCAGGACATCTCCAT
 SEQ ID NO: 9 186 CGTGCCGTCATCGACTTTGTGGCTTCCAGGACATCTCCAT
 SEQ ID NO: 3 451 CGTGCCGTCATCGACTTTGTGGCTTCCAGGACATCTCCAT

Fig. 4 (cont.)

CNA 30942
HNF1R2

MRALLEGPGLSLLCLVLAALPAILLVPAVRGVATIPITYPWFDALIG
MAPVAVWAAALAVGLERWAAAHALPAQVAFIPYAPLPGSICRLREYQQI

CNA 30942
HNF1R2

CRD1 CRD2
45 ERLVCAQCPCPGTFVORPCRRDSPITICGPPPRHYTOFWNYLERCRYCHVL
50 AQMCCKSCSPGQNAKVFCTKISQIVCDSCEDSTYTOIWNWVPECLSGSA

CNA 30942
HNF1R2

CRD2 CRD3
95 CGEREEEARACHATHNRACRCRTGFF...AHAG...FCLEHASCPPGAAGV
100 CSSDQVETOACTREQNRICRCRPGWYCALSKQEGCRLCAPLRKCRPGFGV

CNA 30942
HNF1R2

CRD3 CRD4
139 IAPQTFSQHTQCPQCPGTFSSASSSSSEQCPPHRNCIALGLALNVPSSSS
150 ARPGTETSQVYCKPCAPGTFSSNTSSSTOICRPHQICNVVA...IPGNAS

CNA 30942
HNF1R2

CRD4
189 HDTLCTSCGTGFP LSTRVPGAEECERAVIDFVAFQDISIKRLQRLLOALEA
196 RDAVCTSTS...PTRSNAPGAVHLPOPVSTRSQHTOPTPEPSTAPSTSFL

CNA 30942
HNF1R2

229 PEGWGPPTP...RAGRAALOLKLRRLTELGAQDGALLVRLQALRVAMP
244 PMGSPSPAEGSTGDFALPVGLIVGVIALGLLIIGVVNCVIMTOVKKKPL

CNA 30942
HNF1R2

287 GLERSYRERFLPVH
293 CLOREAKVPHLPADKARGTQGPEQOHLITAPSSSSSSLESSASALORRA

HNF1R2

343 PTRNQPOAPGVEASGAGEARASTGSSDSSPGGHGTQVNVTCIVNVCSSSD

HNF1R2

393 HSSQCSSQASSTMGOTDSSPSES PKDEQVPFSKEECAFRSOLETPETLLG

HNF1R2

443 STEEKPLPLGVPOAGMKPS

Fig. 5

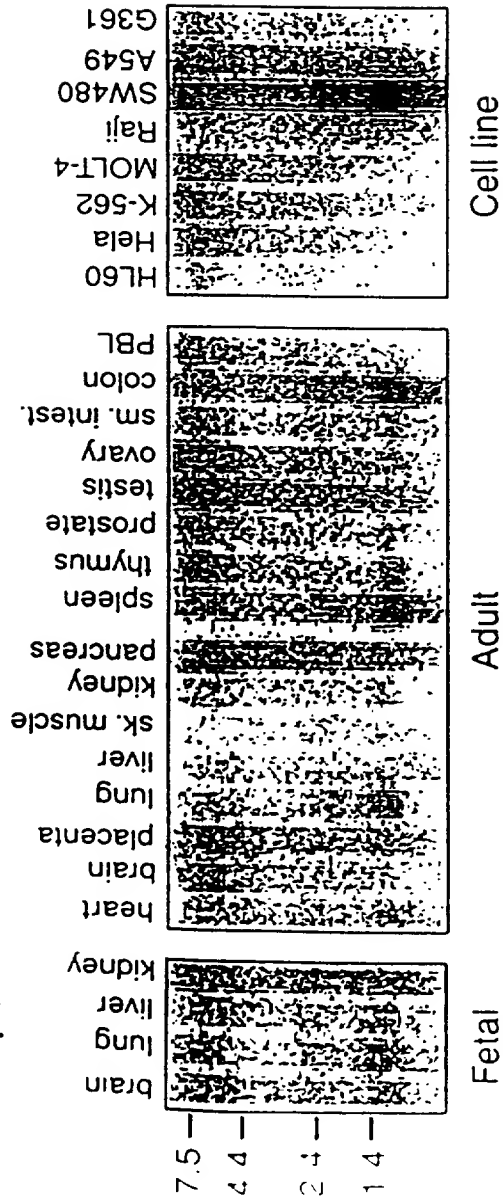


Fig. 7

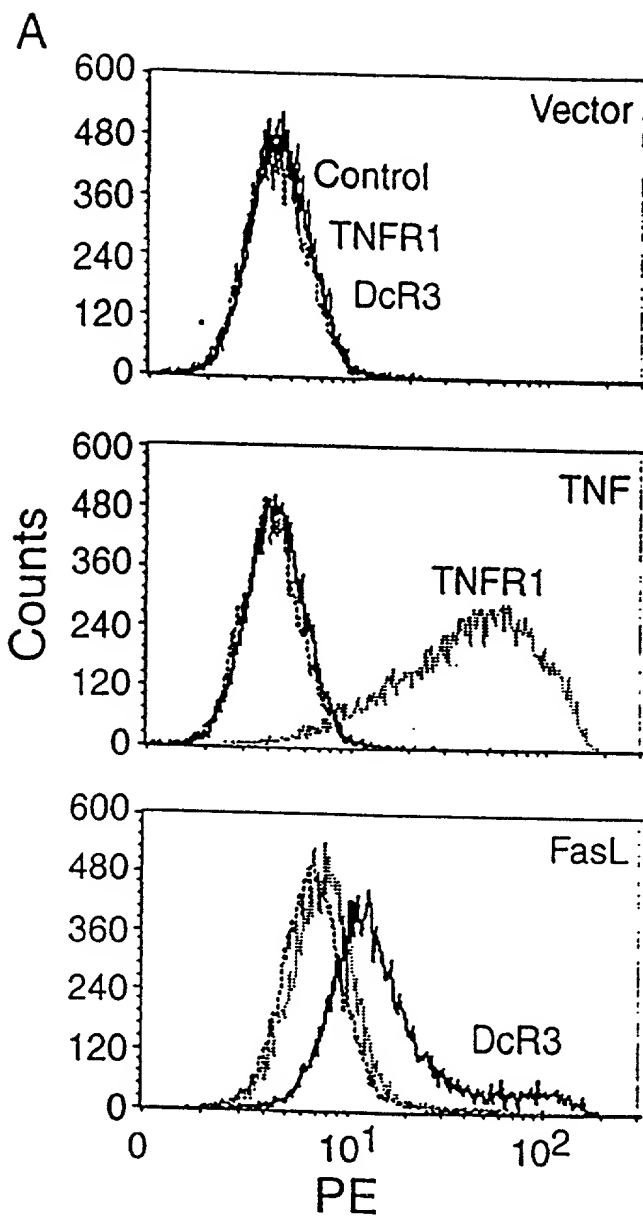
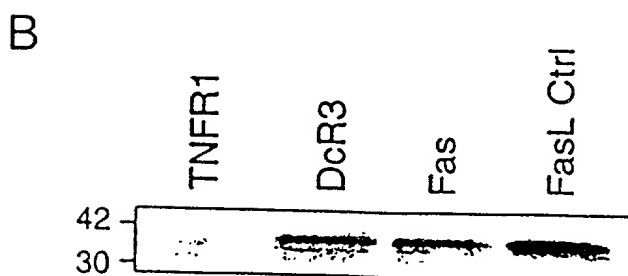


Fig. 8



100390" 96096860

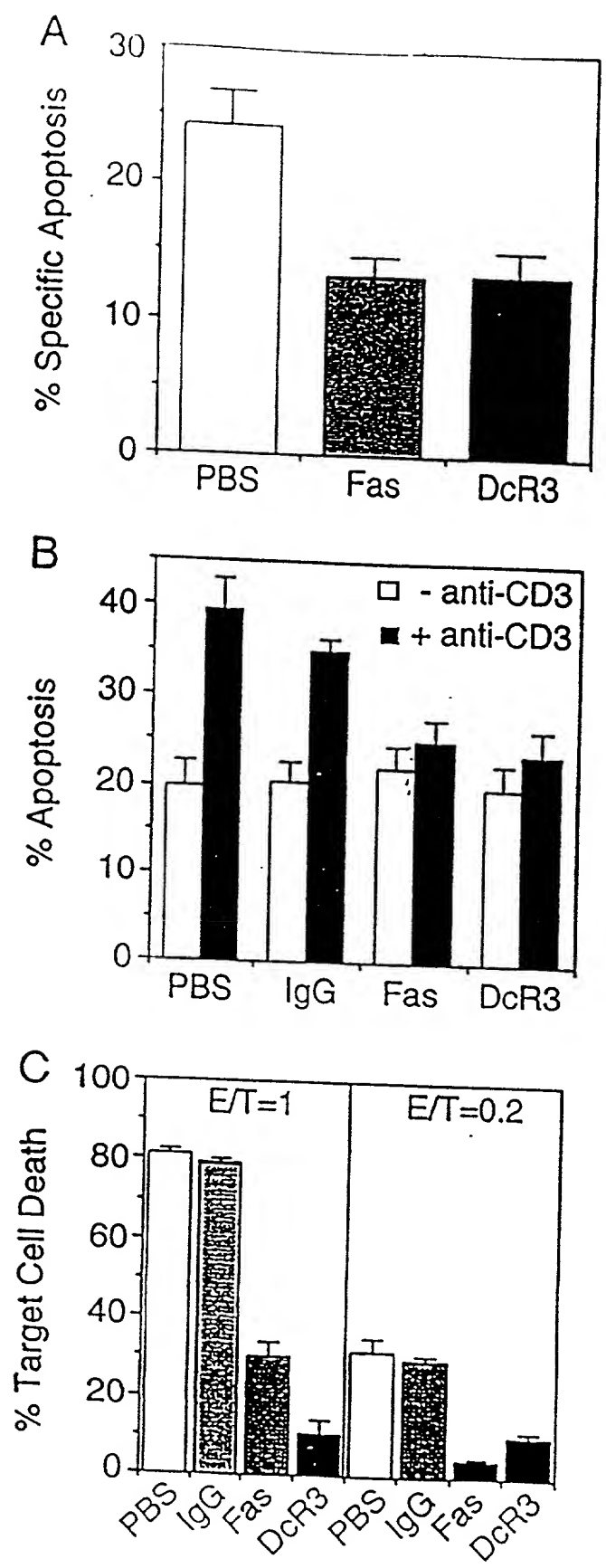


Fig. 9

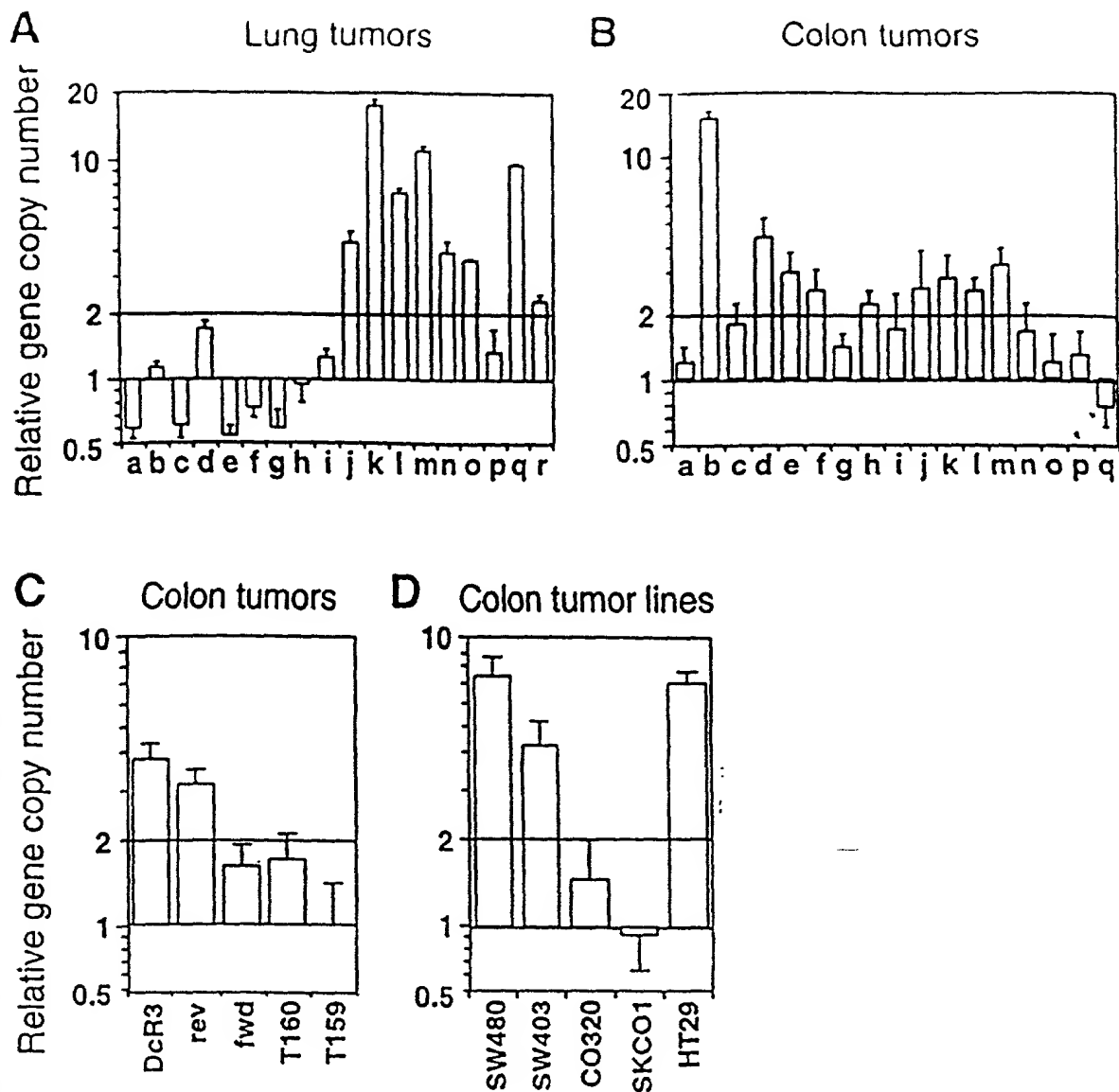


Fig. 10

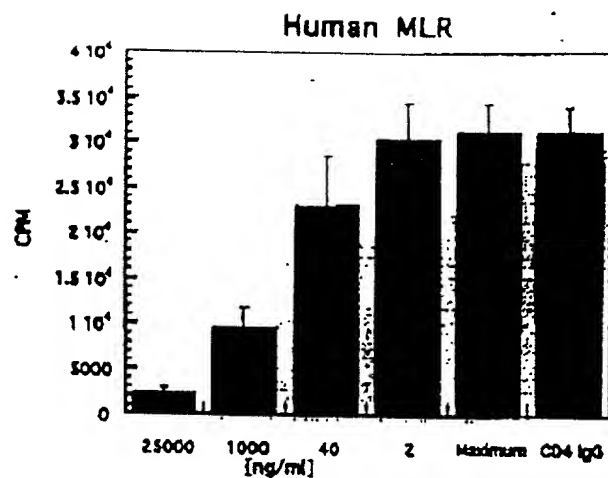


Fig. 11A

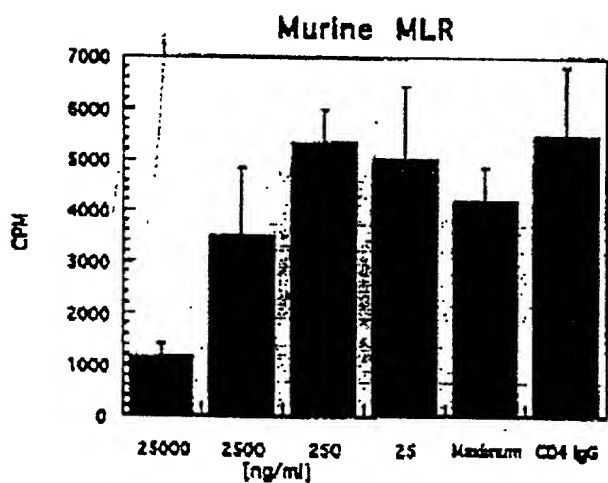


Fig. 11B

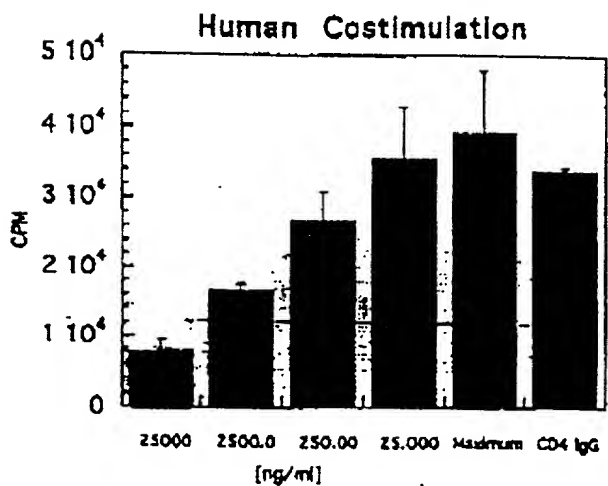


Fig. 11C

FIGURE 12

<u>mAb</u>	<u>Isotype</u>	<u>Antigen Specificity (ELISA)</u>					<u>% Blocking (ELISA)</u>
		<u>DcR3</u>	<u>DR4</u>	<u>DR5</u>	<u>DcR1</u>	<u>OPG</u>	
4B7.1.1	IgG1	+++	-	-	-	-	+
4C4.1.4	IgG2a	+++	-	-	-	-	-
5C4.14.7	IgG2b	+++	-	-	-	-	++
8D3.1.5	IgG1	+++	-	-	-	-	+/-
11C5.2.8	IgG1	+++	-	-	-	-	++

Antigen specificity was determined using 10 microgram/ml mAb.

% blocking activity was determined by ELISA at 100 fold excess of mAb to Fas ligand.

108230-96096850

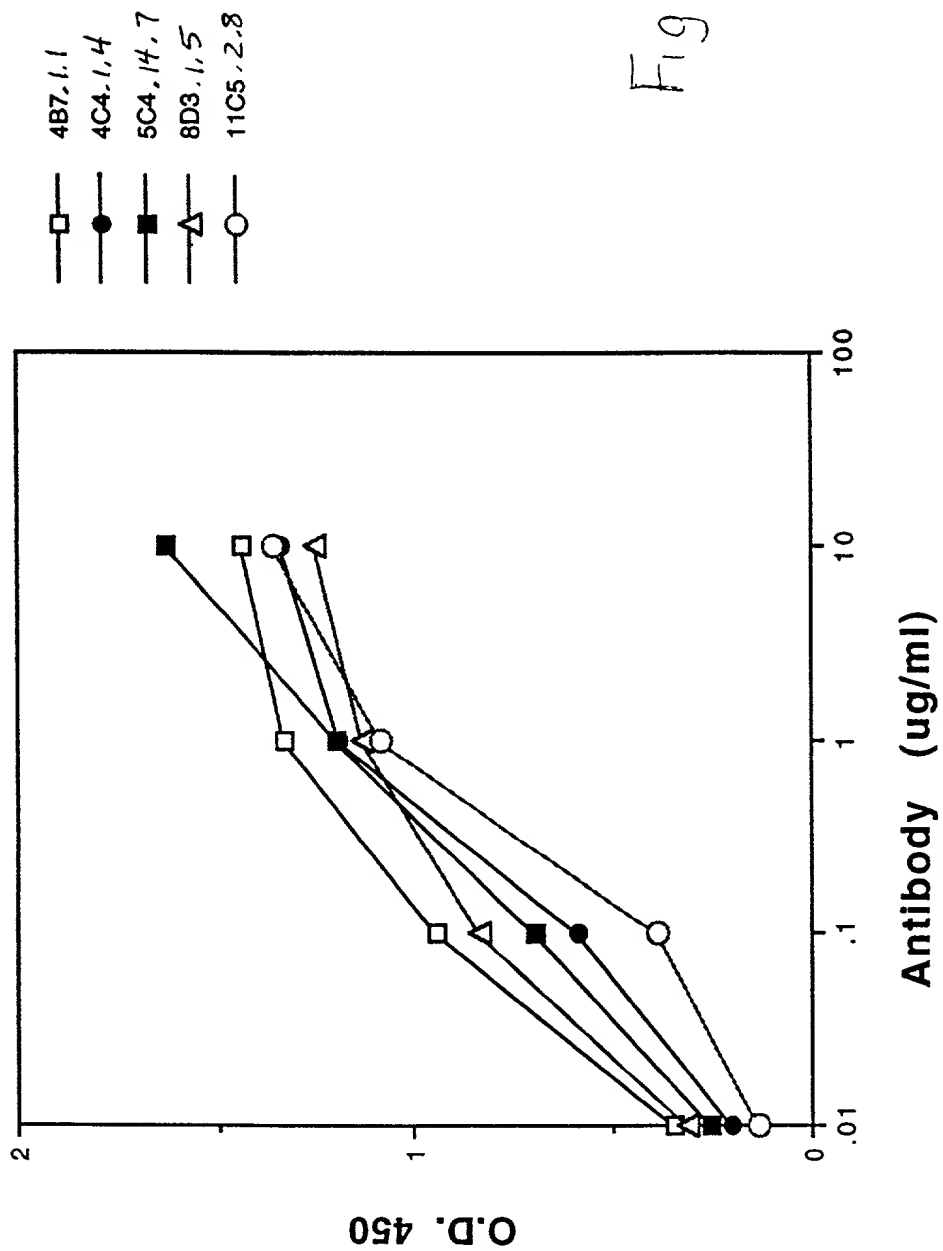


Fig. 13

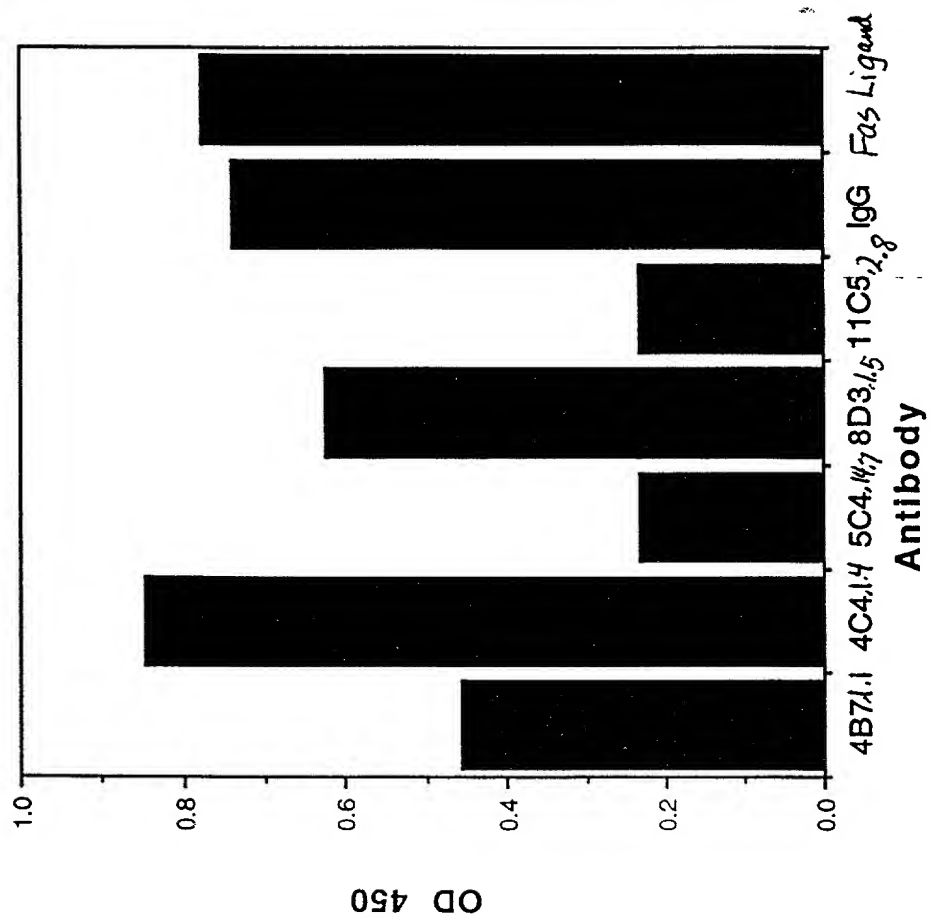


Fig. 14